

AMENDMENT

In the specification:

On page 19 of the specification, please delete the paragraph in the middle of the page starting with the phrase: "Homologues in other organisms are available", and replace it with the following paragraph.

C1
Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package that performs progressive multiples sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol.* 25:351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance between each pair is calculated; from this distance matrix, a guide tree is calculated and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied to encourage the insertion of gaps in probable loop regions instead of in the middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both pairwise alignments and multiple alignments. CLUSTAL W for UNIX and VMS systems is available at: [ftp.ebi.ac.uk](ftp://ftp.ebi.ac.uk). Another program is MACAW (Schuler *et al.*, *Proteins Struct. Func. Genet.* 9:180-190 (1991), the entirety of which is herein incorporated by reference, for which both Macintosh and Microsoft Windows versions are available. MACAW uses a graphical interface, provides a choice of several alignment algorithms and is available by anonymous ftp at: [ncbi.nlm.nih.gov](ftp://ncbi.nlm.nih.gov) (directory/pub/macaw).

On page 66 of the specification, please delete the first paragraph on the page starting with the phrase: "A PCR probe", and replace it with the following paragraph.

C2
A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (www-genome.wi.mit.edu/cgi-bin/www-STS_Pipeline) or GeneUp (Pesole *et al.*, *Biotechniques*